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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/623,596

DATE: 04/30/2001
 TIME: 18:00:49

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\04302001\I623596.raw

3 <110> APPLICANT: WACHI, MASAAKI
 4 NAGAI, KAZUO
 6 <120> TITLE OF INVENTION: A GENE CODING FOR PENICILLIN BINDING PROTEIN AND A METHOD FOR PRODUCING
 7 L-GLUTAMIC ACID
 9 <130> FILE REFERENCE: 196811USOPCT
 11 <140> CURRENT APPLICATION NUMBER: 09/623,596
 12 <141> CURRENT FILING DATE: 2000-09-05
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP99/01084
 15 <151> PRIOR FILING DATE: 1999-03-05
 17 <150> PRIOR APPLICATION NUMBER: JP10-55608
 18 <151> PRIOR FILING DATE: 1998-03-06
 20 <160> NUMBER OF SEQ ID NOS: 6
 22 <170> SOFTWARE: PatentIn version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 5345
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Brevibacterium lactofermentum
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (881)..(2623)
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (2790)..(4454)
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (4467)..(5345)
 41 <400> SEQUENCE: 1
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 44 ggaacaacc cgggccttg tgaaccttg cgtgcagcaa cgcgtaattg atgcagcaca 120
 46 agctgggctc tcagcaggtt atgtcggtgc gtggtcgccc cgttgaggca aaacgtgctg 180
 48 atcctaaggt gatccagctg tctgtgctgg tggttatcct gctgtgcggt ggtgttgccg 240
 50 cgaccatggg tctgtccgga acgtctacac agcagacttt ccagttgcag gaacttcagg 300
 52 caactgaaac ggatttgagc aatcgcatg agtctctcaa ccgagatgtg gaagatgctc 360
 54 gctcagcagc aaccttgcca gcgaatgcta cggagatggg cttggtatcc ccagtggaac 420
 56 ctggcggtgct cgcagtgca gaaaacggtg atgttgtgga ggagcgcgaa caaatccaga 480
 58 gacacgccct atagttgaca tcaatggaca acagaccgga ccaaatcggg catcaagcaa 540
 60 ccctgacgag actaacgcat actgaaaacc tccaggcgat tccacaagaa gcagcagctc 600
 62 cgccgtatca gaccaaacct gttccttatg ctgcaaccac cggacaagca ggtggcgca 660
 64 ggcagtgact ttcccagca atggcagaag tcggggcgag cgtgcgggac gtgaagatac 720
 66 gtcccgccgt tcggcgatc aggacgaaag cagaagagcc gctagagagc gcgaacttac 780
 68 gcgacgcagc ggtaaaagcta aaggcgtaaa ccaagaagaa ggagtgaact accggcctaa 840
 70 atcttcaacc cagggcggcg cagcgaagcg acgtgtgaac atg gtt acc cgt atc 895
 71 Met Val Thr Arg Ile
 72 1 5
 74 gca ttg gtc atc gct ggc gta ctg atc att cgc ctc ggc tgg gtc caa 943
 75 Ala Leu Val Ile Ala Gly Val Leu Ile Ile Arg Leu Gly Trp Val Gln
 76 10 15 20

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78	gtt	gtc	tg	gga	cca	gaa	ctg	tcc	ctc	aat	gct	tcg	gaa	cag	cgc	acc	991
79	Val	Val	Trp	Gly	Pro	Glu	Leu	Ser	Leu	Asn	Ala	Ser	Glu	Gln	Arg	Thr	
80				25					30					35			
82	cgc	gtg	tac	gta	gat	cct	gca	cgc	cgt	gga	acc	atc	gtg	gac	cgc	gaa	1039
83	Arg	Val	Tyr	Val	Asp	Pro	Ala	Arg	Arg	Gly	Thr	Ile	Val	Asp	Arg	Glu	
84		40					45						50				
86	gga	aac	cag	atg	gcg	tac	acg	atg	cag	gca	cgt	tcg	ctg	acg	gtt	tct	1087
87	Gly	Asn	Gln	Met	Ala	Tyr	Thr	Met	Gln	Ala	Arg	Ser	Leu	Thr	Val	Ser	
88		55					60					65					
90	ccg	aac	atc	atg	cgt	gag	gaa	tta	aag	acc	gga	act	gat	ctg	gcc	ttg	1135
91	Pro	Asn	Ile	Met	Arg	Glu	Glu	Leu	Lys	Thr	Gly	Thr	Asp	Leu	Ala	Leu	
92	70					75				80				85			
94	cgt	ttg	gcg	gct	gaa	gaa	acc	gat	ccg	gaa	aac	gtg	gcc	agc	tat	gtg	1183
95	Arg	Leu	Ala	Ala	Glu	Thr	Asp	Pro	Glu	Asn	Val	Ala	Ser	Tyr	Val		
96				90					95				100				
98	acc	atc	gaa	gaa	ggc	aac	gcg	tat	gtt	ttt	gcg	tct	gaa	gaa	cag	cgc	1231
99	Thr	Ile	Glu	Glu	Gly	Asn	Ala	Tyr	Val	Phe	Ala	Ser	Glu	Glu	Gln	Arg	
100				105					110				115				
102	gaa	acc	att	ctg	tcc	gac	aag	gta	gaa	gag	cgt	att	caa	agc	att	gcg	1279
103	Glu	Thr	Ile	Leu	Ser	Asp	Lys	Val	Glu	Glu	Arg	Ile	Gln	Ser	Ile	Ala	
104			120				125						130				
106	gat	cgg	atc	cct	gag	atc	atc	aaa	tcc	cat	gac	caa	gat	gtc	act	gga	1327
107	Asp	Arg	Ile	Pro	Glu	Ile	Ile	Lys	Ser	His	Asp	Gln	Asp	Val	Thr	Gly	
108		135					140					145					
110	att	tcc	tct	gag	gag	atc	ctg	gac	aag	ctc	aat	gca	gat	agc	cag	tat	1375
111	Ile	Ser	Ser	Glu	Glu	Ile	Leu	Asp	Lys	Leu	Asn	Ala	Asp	Ser	Gln	Tyr	
112	150				155					160				165			
114	gag	gtg	ctc	gtc	cgc	aat	gtt	gat	ccc	gat	gta	gcg	tca	gaa	atc	acc	1423
115	Glu	Val	Leu	Val	Arg	Asn	Val	Asp	Pro	Asp	Val	Ala	Ser	Glu	Ile	Thr	
116				170					175				180				
118	gat	gag	atg	ccc	agc	gtc	gca	gct	gat	cat	caa	gac	atc	cgc	caa	tac	1471
119	Asp	Glu	Met	Pro	Ser	Val	Ala	Ala	Asp	His	Gln	Asp	Ile	Arg	Gln	Tyr	
120			185						190				195				
122	cca	aac	ggc	gcg	att	ggt	gaa	aac	atc	atc	ggt	cga	atc	agc	atg	gac	1519
123	Pro	Asn	Gly	Ala	Ile	Gly	Glu	Asn	Ile	Ile	Gly	Arg	Ile	Ser	Met	Asp	
124		200					205					210					
126	ggc	gaa	ggc	cag	ttc	ggc	ttt	gag	gct	tcc	aac	gat	tcc	ctg	ttg	gca	1567
127	Gly	Glu	Gly	Gln	Phe	Gly	Phe	Glu	Ala	Ser	Asn	Asp	Ser	Leu	Leu	Ala	
128		215				220						225					
130	gga	aac	aac	ggt	cgc	tca	acc	cag	gac	atg	tcc	att	ttg	gga	caa	gca	1615
131	Gly	Asn	Asn	Gly	Arg	Ser	Thr	Gln	Asp	Met	Ser	Ile	Leu	Gly	Gln	Ala	
132	230				235					240			245				
134	atc	ccg	ggc	acg	ttg	agg	gat	caa	att	cca	gcc	att	gat	ggt	gcc	agc	1663
135	Ile	Pro	Gly	Thr	Leu	Arg	Asp	Gln	Ile	Pro	Ala	Ile	Asp	Gly	Ala	Ser	
136			250						255				260				
138	gtt	gaa	ctc	acc	gtt	gat	ctg	gat	ctg	caa	acc	tat	gtg	cag	cag	gca	1711
139	Val	Glu	Leu	Thr	Val	Asp	Leu	Asp	Leu	Gln	Thr	Tyr	Val	Gln	Gln	Ala	
140			265						270				275				
142	ttg	gag	cag	gcg	aaa	gct	aac	tcc	ggt	gca	gaa	aac	gcc	tcc	gct	gtg	1759

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143	Leu	Glu	Gln	Ala	Lys	Ala	Asn	Ser	Gly	Ala	Glu	Asn	Ala	Ser	Ala	Val	
144			280					285					290				
146	gtt	ctt	gat	gcc	gag	acc	gct	gag	gtt	ttg	gcg	atg	gca	aac	acc	gat	1807
147	Val	Leu	Asp	Ala	Glu	Thr	Ala	Glu	Val	Leu	Ala	Met	Ala	Asn	Thr	Asp	
148		295					300					305					
150	acc	atc	aac	ccc	aac	gaa	gac	acg	gga	aag	cag	att	gag	cag	ggc	aag	1855
151	Thr	Ile	Asn	Pro	Asn	Glu	Asp	Thr	Gly	Lys	Gln	Ile	Glu	Gln	Gly	Lys	
152	310					315					320				325		
154	agc	ttt	gac	aat	cct	tct	gtc	acc	cac	ccc	ttc	gag	cct	ggt	tct	gta	1903
155	Ser	Phe	Asp	Asn	Pro	Ser	Val	Thr	His	Pro	Phe	Glu	Pro	Gly	Ser	Val	
156				330						335				340			
158	gcc	aag	gtg	att	act	gca	gca	ggc	gta	att	caa	gac	ggc	ttg	act	act	1951
159	Ala	Lys	Val	Ile	Thr	Ala	Ala	Gly	Val	Ile	Gln	Asp	Gly	Leu	Thr	Thr	
160			345						350					355			
162	cca	gat	gaa	gtg	ttg	cag	gta	ccg	ggc	agt	att	gaa	atg	gcc	ggt	gtt	1999
163	Pro	Asp	Glu	Val	Leu	Gln	Val	Pro	Gly	Ser	Ile	Glu	Met	Ala	Gly	Val	
164		360						365				370					
166	tct	gtc	ggt	gat	gcg	tgg	gac	cac	ggt	gtc	gtt	ccc	tat	acc	act	gca	2047
167	Ser	Val	Gly	Asp	Ala	Trp	Asp	His	Gly	Val	Val	Pro	Tyr	Thr	Thr	Ala	
168		375					380					385					
170	gga	att	ttt	ggt	aag	tcc	tcg	aat	gta	ggc	act	ctg	atg	ctt	gcg	cac	2095
171	Gly	Ile	Phe	Gly	Lys	Ser	Ser	Asn	Val	Gly	Thr	Leu	Met	Leu	Ala	His	
172	390					395					400				405		
174	ggt	ctt	ggt	gaa	gat	aaa	ttt	gct	gat	tac	ctg	gaa	cga	ttc	ggt	gtg	2143
175	Gly	Leu	Gly	Glu	Asp	Lys	Phe	Ala	Asp	Tyr	Leu	Glu	Arg	Phe	Gly	Val	
176			410						415					420			
178	gga	cag	tca	acg	ggt	att	gag	ctt	ccg	agc	gaa	tcc	caa	ggc	ctg	ctg	2191
179	Gly	Gln	Ser	Thr	Gly	Ile	Glu	Leu	Pro	Ser	Glu	Ser	Gln	Gly	Leu	Leu	
180			425						430				435				
182	ccc	gca	cgt	gag	cag	tgg	tct	ggc	ggt	act	ttt	gct	aac	ctg	ccc	atc	2239
183	Pro	Ala	Arg	Glu	Gln	Trp	Ser	Gly	Gly	Thr	Phe	Ala	Asn	Leu	Pro	Ile	
184		440					445					450					
186	ggt	cag	ggt	atg	tcg	atc	acc	acg	ttg	caa	atg	gct	gga	atc	tac	caa	2287
187	Gly	Gln	Gly	Met	Ser	Ile	Thr	Thr	Leu	Gln	Met	Ala	Gly	Ile	Tyr	Gln	
188		455				460					465						
190	gcc	ttg	gcc	aac	gat	ggt	gaa	cgc	att	gaa	ccg	cgg	atc	atc	aag	agc	2335
191	Ala	Leu	Ala	Asn	Asp	Gly	Glu	Arg	Ile	Glu	Pro	Arg	Ile	Ile	Lys	Ser	
192	470				475					480				485			
194	gtg	act	gat	tct	gac	gga	aca	gtc	cta	gag	cag	ccg	gaa	ccc	gat	aaa	2383
195	Val	Thr	Asp	Ser	Asp	Gly	Thr	Val	Leu	Glu	Gln	Pro	Glu	Pro	Asp	Lys	
196			490						495				500				
198	atc	cag	gtt	gtc	agc	gct	gaa	gct	gcc	cgc	acc	acg	gtg	gat	atg	ttt	2431
199	Ile	Gln	Val	Val	Ser	Ala	Glu	Ala	Ala	Arg	Thr	Thr	Val	Asp	Met	Phe	
200			505						510				515				
202	agg	tct	gtc	acc	cag	gtt	gat	cca	ctt	gga	gtg	cac	aag	gta	ccg	ctc	2479
203	Arg	Ser	Val	Thr	Gln	Val	Asp	Pro	Leu	Gly	Val	His	Lys	Val	Pro	Leu	
204		520					525				530						
206	cag	acg	cct	cca	ttg	agg	gtt	atc	aaa	tct	cag	gta	aga	cag	gta	cgg	2527
207	Gln	Thr	Pro	Pro	Leu	Arg	Val	Ile	Lys	Ser	Gln	Val	Arg	Gln	Val	Arg	

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208	535	540	545	
210	cgc aaa aag ttg acc cca aca cgg gcg cgt act cta act cgc aat act			2575
211	Arg Lys Lys Leu Thr Pro Thr Arg Ala Arg Thr Leu Thr Arg Asn Thr			
212	550	555	560	565
214	gga tta cct tct cgg gta ttg cac cgg ctg atg atc ctc gat ttg ttg			2623
215	Gly Leu Pro Ser Arg Val Leu His Pro Leu Met Ile Leu Asp Leu Leu			
216		570	575	580
218	tagccatcat gcttgatgag ccagaacgcg gagtccacgg tgggtggcggc caaaccgcag			2683
220	cacctttggt caaagacatc gccacctggt tgctcaaccg cgacaacatc ccaactgtctg			2743
222	cagccaccga accgatcatc ctccaagctc aataactcaa acagaa gtg tct ttt			2798
223				Val Ser Phe
226	gta gaa ttt cat aat ctg aac ttt tgt ttg aac tct ttt cgg cat cac			2846
227	Val Glu Phe His Asn Leu Asn Phe Cys Leu Asn Ser Phe Arg His His			
228	585	590	595	600
230	cca cgt gcc gcg tcc gaa tta tta aca cct aga aac ctg tgg agg aga			2894
231	Pro Arg Ala Ala Ser Glu Leu Leu Thr Pro Arg Asn Leu Trp Arg Arg			
232		605	610	615
234	gaa aac cat ggc aac cac gtt gct gga cct cac caa act tat cga tgg			2942
235	Glu Asn His Gly Asn His Val Ala Gly Pro His Gln Thr Tyr Arg Trp			
236		620	625	630
238	cat cct caa ggg ctc tgc cag ggc gtt ccc gct cac gca gta ggg gaa			2990
239	His Pro Gln Gly Leu Cys Gln Gly Val Pro Ala His Ala Val Gly Glu			
240		635	640	645
242	caa gca atc gcg gct att ggt ctt gac tcc tcc agc ttg cct acc tcg			3038
243	Gln Ala Ile Ala Ala Ile Gly Leu Asp Ser Ser Leu Pro Thr Ser			
244		650	655	660
246	gac gct att ttt gct gca gtt cca gga acc cgc act cac ggc gca cag			3086
247	Asp Ala Ile Phe Ala Ala Val Pro Gly Thr Arg Thr His Gly Ala Gln			
248	665	670	675	680
250	ttt gca ggt acg gat aac gct gcg aaa gct gtg gcc att ttg act gac			3134
251	Phe Ala Gly Thr Asp Asn Ala Ala Lys Ala Val Ala Ile Leu Thr Asp			
252		685	690	695
254	gca gct gga ctt gag gtg ctc aac gaa gca gga gag acc cgc cca atc			3182
255	Ala Ala Gly Leu Glu Val Leu Asn Glu Ala Gly Glu Thr Arg Pro Ile			
256		700	705	710
258	atc gtt gtt gat gat gtc cgc gca gta ctt ggc gca gca tca tca agc			3230
259	Ile Val Val Asp Asp Val Arg Ala Val Leu Gly Ala Ala Ser Ser Ser			
260		715	720	725
262	att tat ggc gat cct tca aaa gat ttc acg ctc att gga gtc act gga			3278
263	Ile Tyr Gly Asp Pro Ser Lys Asp Phe Thr Leu Ile Gly Val Thr Gly			
264		730	735	740
266	acc tca ggt aaa acc acc acc agc tac ctc ttg gaa aaa gga ctc atg			3326
267	Thr Ser Gly Lys Thr Thr Thr Ser Tyr Leu Leu Glu Lys Gly Leu Met			
268	745	750	755	760
270	gag gca ggc cac aaa gtt ggt ttg atc ggc acc aca ggt aca cgt ata			3374
271	Glu Ala Gly His Lys Val Gly Leu Ile Gly Thr Thr Gly Thr Arg Ile			
272		765	770	775
274	gat ggg gaa gaa gta ccc acg aag ctc acc act cca gaa gcg ccg act			3422
275	Asp Gly Glu Glu Val Pro Thr Lys Leu Thr Thr Pro Glu Ala Pro Thr			

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278	ctg	cag	gca	ttg	ttt	gct	cga	atg
279	Leu	Gln	Ala	Leu	Phe	Ala	Arg	Met
280								
282	gtg	atg	gaa	gta	tcc	agc	cat	gca
283	Val	Met	Glu	Val	Ser	Ser	His	Ala
284								
286	tcc	cac	ttt	gat	gta	gct	gcg	ttt
287	Ser	His	Phe	Asp	Val	Ala	Ala	Phe
288								
290	gat	ttc	cac	ccc	acc	atg	gat	gat
291	Asp	Phe	His	Pro	Thr	Met	Asp	Asp
292								
294	ttc	cg	gca	gat	tct	cca	ctt	gtg
295	Phe	Arg	Ala	Asp	Ser	Pro	Leu	Val
296								
298	gat	gat	tct	tgg	ggt	cag	cg	atg
299	Asp	Asp	Ser	Trp	Gly	Gln	Arg	Met
300								
302	aca	gta	tcc	acc	ctt	ggg	caa	gaa
303	Thr	Val	Ser	Thr	Leu	Gly	Gln	Glu
304								
306	aat	gtc	agc	gac	tct	ggc	gcc	cag
307	Asn	Val	Ser	Asp	Ser	Gly	Ala	Gln
308								
310	aac	cag	tcc	tac	cag	gtc	gag	cta
311	Asn	Gln	Ser	Tyr	Gln	Val	Glu	Leu
312								
314	gct	aac	gcc	acg	ttg	gca	ttt	gcc
315	Ala	Asn	Ala	Thr	Leu	Ala	Phe	Ala
316								
318	gcg	acg	ttt	gct	cga	ggc	atg	tcc
319	Ala	Thr	Phe	Ala	Arg	Gly	Met	Ser
320								
322	gaa	cg	att	gat	gag	gga	caa	gac
323	Glu	Arg	Ile	Asp	Glu	Gly	Gln	Asp
324								
326	cac	aag	cct	gct	gca	gtg	gct	gct
327	His	Lys	Pro	Ala	Ala	Val	Ala	Ala
328								
330	att	gac	ggg	cg	ctc	gga	agt	ggt
331	Ile	Asp	Gly	Arg	Leu	Gly	Ser	Gly
332								
334	gat	tcc	acc	aag	cgt	ggc	ccc	atg
335	Asp	Ser	Thr	Lys	Arg	Gly	Pro	Met
336								
338	gga	tct	agt	tat	tgt	act	gat	gca
339	Gly	Ser	Ser	Tyr	Cys	Thr	Asp	Ala
340								

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